










































Related Structures

Sequences producing significant alignments:			Score (bits)	E Value	
gi 6912284 ref NP_036245.1 	carbonic anhydrase XIV precursor...	682	0.0	L	
gi 22760422 dbj BAC11191.1 	unnamed protein product [Homo s...	681	0.0	L	
gi 6753264 ref NP_035927.1 	carbonic anhydrase 14; CA XIV [...	548	e-155	L	
gi 47168790 pdb 1R35 A	Chain A, Crystal Structure of The Ex...	438	e-122	S	
gi 21431756 sp Q9MZ30 CAHC_RABIT	Carbonic anhydrase XII pre...	270	3e-71		
gi 4502515 ref NP_001209.1 	carbonic anhydrase XII isoform ...	264	2e-69	L	
gi 30585185 gb AAP36865.1 	Homo sapiens carbonic anhydrase ...	263	5e-69		
gi 45935383 ref NP_996808.1 	carbonic anhydrase XII isoform...	263	5e-69	L	
gi 26342835 dbj BAC35074.1 	unnamed protein product [Mus mu...	262	9e-69	L	
gi 31541884 ref NP_848483.2 	carbonic anyhydrase 12 [Mus mu...	261	1e-68	L	
gi 34864283 ref XP_343417.1 	similar to 2310047E01Rik prote...	261	1e-68	L	
gi 47221597 emb CAF97862.1 	unnamed protein product [Tetrao...	261	2e-68		
gi 21595173 gb AAH31385.1 	Car12 protein [Mus musculus]	260	3e-68	L	
gi 47225853 emb CAF98333.1 	unnamed protein product [Tetrao...	254	1e-66		
gi 34858063 ref XP_342298.1 	similar to CA XIV [Rattus norv...	246	4e-64	L	
gi 15826782 pdb 1JCZ A	Chain A, Crystal Structure of The Ex...	246	6e-64	S	
gi 47211349 emb CAF93821.1 	unnamed protein product [Tetrao...	240	3e-62		
gi 47228789 emb CAG07521.1 	unnamed protein product [Tetrao...	236	4e-61		
gi 49117984 gb AAH72918.1 	Unknown (protein for MGC:80389) ...	209	5e-53		
gi 9955948 ref NP_001207.1 	carbonic anhydrase IX precursor...	203	4e-51	L	
gi 21314850 ref NP_647466.1 	carbonic anhydrase 9 [Mus musc...	201	2e-50	L	
gi 30580354 sp Q8VHB5 CAH9_MOUSE	Carbonic anhydrase IX prec...	201	2e-50	L	
gi 115469 sp P08060 CAH6_SHEEP	Carbonic anhydrase VI (Carbo...	197	2e-49		
gi 89853 pir A29993	carbonate dehydratase (EC 4.2.1.1) VI ...	197	4e-49		
gi 34935135 ref XP_233380.2 	similar to carbonic anhydrase ...	196	5e-49	L	
gi 27806915 ref NP_776323.1 	carbonic anhydrase VI [Bos tau...	195	1e-48	L	
gi 28812184 dbj BAC65098.1 	carbonic anhydrase VI [Canis fa...	189	6e-47	L	
gi 14530767 emb CAC42429.1 	dJ477M7.5 (carbonic anhydrase V...	186	5e-46	L	
gi 1070519 pir CRHU6	carbonate dehydratase (EC 4.2.1.1) VI...	184	3e-45		
gi 23503046 sp P23280 CAH6_HUMAN	Carbonic anhydrase VI prec...	181	1e-44	L	
gi 4557397 ref NP_001206.1 	carbonic anhydrase VI precursor...	181	2e-44	L	
gi 31076619 sp Q8UWA5 CAH2_TRIHK	Carbonic anhydrase II (Car...	180	5e-44		
gi 34872490 ref XP_216584.2 	similar to Car6 protein [Rattu...	179	7e-44	L	
gi 40363537 ref NP_954685.1 	carbonic anhydrase II [Danio r...	177	3e-43	L	
gi 29789369 ref NP_599183.1 	protein tyrosine phosphatase, ...	176	6e-43	L	
gi 25281969 gb AAN72430.1 	receptor-like protein tyrosine p...	176	6e-43	L	
gi 6679559 ref NP_033007.1 	protein tyrosine phosphatase, r...	176	7e-43	L	
gi 25281971 gb AAN72431.1 	receptor-like protein tyrosine p...	176	1e-42	L	
gi 45709528 gb AAH67635.1 	LOC407683 protein [Danio rerio]	174	2e-42	L	
gi 45383516 ref NP_989645.1 	protein tyrosine phosphatase, ...	174	2e-42	L	
gi 18860898 ref NP_002832.2 	protein tyrosine phosphatase, ...	174	3e-42	L	
gi 1263069 gb AAC50439.1 	receptor tyrosine phosphatase gam...	174	3e-42	L	
gi 477137 pir A48148	protein-tyrosine-phosphatase (EC 3.1....	173	5e-42		
gi 25281973 gb AAN72432.1 	receptor-like protein tyrosine p...	172	7e-42	L	
gi 41387130 ref NP_957107.1 	hypothetical protein MGC73385 ...	172	1e-41	L	
gi 29179452 gb AAH49309.1 	Zgc:73385 protein [Danio rerio]	169	1e-40	L	
gi 5921196 sp P18761 CAH6_MOUSE	Carbonic anhydrase VI precu...	168	1e-40	L	
gi 33585712 gb AAH55437.1 	Car6 protein [Mus musculus]	166	9e-40	L	
gi 29612611 gb AAH49973.1 	Car6 protein [Mus musculus]	166	9e-40	L	
gi 50418465 gb AAH78387.1 	Unknown (protein for IMAGE:70369...	164	3e-39		
gi 34851195 ref XP_226204.2 	similar to carbonic anhydrase ...	161	2e-38	L	
gi 68286 pir CRRB2	carbonate dehydratase (EC 4.2.1.1) II -...	161	2e-38		

gi 2098445 pdb 1UGF	Human Carbonic Anhydrase Ii [hcai]	(...	161	3e-38	
gi 28269695 ref NP_444300.1	carbonic anhydrase 7; carbonic...		160	4e-38	
gi 47227809 emb CAG08972.1	unnamed protein product [Tetrao...		159	7e-38	
gi 4557395 ref NP_000058.1	carbonic anhydrase II; carbonat...		159	7e-38	
gi 1942501 pdb 1UGD	Human Carbonic Anhydrase Ii[hcai]	(E...	159	7e-38	
gi 2118910 pir A48993	protein-tyrosine-phosphatase (EC 3.1...		159	9e-38	
gi 11513906 pdb 1G3Z A	Chain A, Carbonic Anhydrase Ii (F131...		159	1e-37	
gi 15080386 gb AAH11949.1	Carbonic anhydrase II [Homo sapi...		159	1e-37	
gi 229731 pdb 1CA2	Carbonic Anhydrase II (Carbonate Dehyd...		159	1e-37	
gi 442669 pdb 1BCD	Carbonic Anhydrase Ii (E.C.4.2.1.1) Co...		159	1e-37	
gi 1421269 pdb 1CAN	Carbonic Anhydrase Ii (E.C.4.2.1.1) C...		159	1e-37	
gi 1942500 pdb 1UGB	Human Carbonic Anhydrase Ii[hcai]	(E...	159	1e-37	
gi 38348436 ref NP_940986.1	carbonic anhydrase XIII; carbo...		159	1e-37	
gi 1942499 pdb 1UGA	Human Carbonic Anhydrase Ii[hcai]	(E...	159	1e-37	
gi 2098448 pdb 1UGE	Human Carbonic Anhydrase Ii [hcai]	(...	159	1e-37	
gi 115448 sp P00917 CAH1_HORSE	Carbonic anhydrase I (Carbon...		158	1e-37	
gi 22219225 pdb 1LG5 A	Chain A, Crystal Structure Analysis ...		158	1e-37	
gi 2098447 pdb 1UGC	Human Carbonic Anhydrase Ii [hcai]	(...	158	2e-37	
gi 22252956 gb AAM94169.1	erythrocyte carbonic anhydrase [...		158	2e-37	
gi 68288 pir CRBO2	carbonate dehydratase (EC 4.2.1.1) II -...		158	2e-37	
gi 442701 pdb 1CAJ	Carbonic Anhydrase Ii (E.C.4.2.1.1) Mu...		158	2e-37	
gi 1065006 pdb 1CNH	Carbonic Anhydrase Ii (Carbonate Dehy...		158	2e-37	
gi 999629 pdb 1YDB	Carbonic Anhydrase Ii (Carbonate Dehyd...		158	2e-37	
gi 231119 pdb 5CA2	Carbonic Anhydrase II (Carbonate Dehyd...		157	2e-37	
gi 1633065 pdb 1ZSC	Carbonic Anhydrase Ii Mutant E117q, H...		157	3e-37	
gi 442702 pdb 1CAK	Carbonic Anhydrase Ii (E.C.4.2.1.1) Mu...		157	3e-37	
gi 46048696 ref NP_990648.1	carbonic anhydrase II [Gallus ...		157	3e-37	
gi 231199 pdb 6CA2	Carbonic Anhydrase II (Carbonate Dehyd...		157	3e-37	
gi 442772 pdb 1CVA	Carbonic Anhydrase Ii (Hca Ii) (E.C.4....		157	3e-37	
gi 442826 pdb 1DCA	Carbonic Anhydrase II (Carbonate Dehyd...		157	3e-37	
gi 1065012 pdb 1CNJ	Carbonic Anhydrase Ii (Carbonate Dehy...		157	3e-37	
gi 1345651 sp P48282 CAH1_SHEEP	Carbonic anhydrase I (Carbo...		157	3e-37	
gi 229981 pdb 1HED	Carbonic Anhydrase II (Carbonate Dehyd...		157	3e-37	
gi 442703 pdb 1CAL	Carbonic Anhydrase Ii (E.C.4.2.1.1) Mu...		157	3e-37	
gi 229657 pdb 12CA	Carbonic Anhydrase II (Carbonate Dehyd...		157	3e-37	
gi 1065011 pdb 1CNI	Carbonic Anhydrase Ii (Carbonate Dehy...		157	3e-37	
gi 999932 pdb 1CCS	Carbonic Anhydrase Ii (Carbonate Dehyd...		157	4e-37	
gi 1065001 pdb 1CNG	Carbonic Anhydrase Ii (Carbonate Dehy...		157	4e-37	
gi 442700 pdb 1CAI	Carbonic Anhydrase Ii (E.C.4.2.1.1) Mu...		157	4e-37	
gi 229978 pdb 1HEA	Carbonic Anhydrase II (Carbonate Dehyd...		157	4e-37	
gi 999632 pdb 1YDD	Carbonic Anhydrase Ii (Carbonate Dehyd...		157	4e-37	
gi 2554664 pdb 1H9N	H119n Carbonic Anhydrase Ii		157	4e-37	
gi 2554643 pdb 2H4N	H94n Carbonic Anhydrase Ii Complexed ...		157	4e-37	
gi 24987658 pdb 1LZV A	Chain A, Site-Specific Mutant (Tyr7 ...		157	4e-37	
gi 231320 pdb 9CA2	Carbonic Anhydrase II (Carbonate Dehyd...		157	4e-37	
gi 1168741 sp P00919 CAH2_RABIT	Carbonic anhydrase II (Carb...		157	5e-37	
gi 999935 pdb 1CCT	Carbonic Anhydrase Ii (Carbonate Dehyd...		156	5e-37	
gi 1289219 emb CAA29417.1	carbonic anhydrase II [Gallus ga...		156	5e-37	

Alignments

Get selected sequences

Select all

Deselect all

>gi|6912284|ref|NP_036245.1| carbonic anhydrase XIV precursor; carbonic dehydratase [Homo sapiens]

gi|8928036|sp|Q9ULX7|CAHE_HUMAN Carbonic anhydrase XIV precursor (Carbonate dehydratase XIV (CA-XIV) (UNQ690/PRO1335)

gi|6009640|dbj|BAA85002.1| carbonic anhydrase 14 [Homo sapiens]

gi|21706779|gb|AAH34412.1| Carbonic anhydrase XIV, precursor [Homo sapiens]

gi|37182500|gb|AAQ89052.1| CA14 [Homo sapiens]

Length = 337

Score = 682 bits (1760), Expect = 0.0

Identities = 337/337 (100%), Positives = 337/337 (100%)

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Query: 1  MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60
          MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD
Sbjct: 1  MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60

Query: 61  LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120
          LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG
Sbjct: 61  LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120

Query: 121 SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180
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Sbjct: 121 SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180

Query: 181 LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240
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Sbjct: 181 LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240

Query: 241 LEKLQGTLLFSTEEEPSKLLVQNYRALQPLNQRMFASFQAGSSYTTGEMLSLGVGILVG 300
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Sbjct: 241 LEKLQGTLLFSTEEEPSKLLVQNYRALQPLNQRMFASFQAGSSYTTGEMLSLGVGILVG 300

Query: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337
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>gi|22760422|dbj|BAC11191.1| unnamed protein product [Homo sapiens]
Length = 337

Score = 681 bits (1756), Expect = 0.0

Identities = 336/337 (99%), Positives = 336/337 (99%)

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Sbjct: 1  MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60

Query: 61  LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120
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Sbjct: 61  LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120

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Query: 181 LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240
          LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ
Sbjct: 181 LHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240

Query: 241 LEKLQGTLLFSTEEEPSKLLVQNYRALQPLNQRMFASFQAGSSYTTGEMLSLGVGILVG 300
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Sbjct: 241 LEKLQGTLLFSTEEEPSKLLVQNYRALQPLNQRMFASFQAGSSYTTGEMLSLGVGILVG 300

Query: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337
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Sbjct: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337

```

>gi|6753264|ref|NP_035927.1| carbonic anhydrase 14; CA XIV [Mus musculus]
 gi|8928038|sp|Q9WVT6|CAHE_MOUSE Carbonic anhydrase XIV precursor (Carbonate dehydratase XIV (CA-XIV))
 gi|5030908|dbj|BAA78709.1| CA XIV [Mus musculus]
 gi|28422260|gb|AAH46995.1| Carbonic anhydrase 14 [Mus musculus]
 Length = 337

Score = 548 bits (1413), Expect = e-155
 Identities = 283/337 (83%), Positives = 306/337 (90%)

Query: 1 MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60
 MLF ALLL+V WILAADGG HWTYEGPHGQDHP SYPECG +AQSPI+IQTDSV FDPD
 Sbjct: 1 MLFFALLLKVTWILAADGGHHWTYEGPHGQDHWPTSYPECGGDAQSPINIQTDSVIFDPD 60

Query: 61 LPALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120
 LPA+QPHGYDQ GTEPLDLHNNGHTVQLSLP TL+LGGLPRKY AAQLHLHWGQ+GS G
 Sbjct: 61 LPAVQPHGYDQLGTEPLDLHNNGHTVQLSLPPTLHLGGLPRKYTAAQLHLHWGQRGSLEG 120

Query: 121 SEHQINSEATFAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180
 SEHQINSEAT AELH+VHYDS SY SLSEAA++PQGLAVLGILIEVGET+N AY+HILS
 Sbjct: 121 SEHQINSEATAAELHVHYDSQSYSSLSEAAQKPQGLAVLGILIEVGETENPAYDHILSR 180

Query: 181 LHEVRHKDQKTSVPPFNRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240
 LHE+R+KDQKTSVPPF++REL P+QL Q+FRYNGSLTTPPCYQSVLWTVF RR+QISM Q
 Sbjct: 181 LHEIRYKDQKTSVPPFSVRELFPQLEQFFRYNGSLTTPPCYQSVLWTVFNRAQISMGG 240

Query: 241 LEKLQGTLFSTEEEPSKLLVQNYRALQPLNQRMFASFQAGSSYTTGEMLSLGVGILVG 300
 LEKLQ TL STEE+PS+ LVQNYR QPLNQR +FASFQAG YTTGEML LGVGIL G
 Sbjct: 241 LEKLQETLSSTEEDPSEPLVQNYRVPQPLNQRRTIFASFQAGPLYTTGEMLGLGVGILAG 300

Query: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337
 CLCLLLAVYFIA+KIRKKRL NRKSVVFTSA+ATTEA
 Sbjct: 301 CLCLLLAVYFIAQKIRKKRLGNRKSVVFTSARATTEA 337

>gi|47168790|pdb|1RJ5|A Chain A, Crystal structure of The Extracellular Domain of Murine Carbonic Anhydrase Xiv
 gi|47168791|pdb|1RJ5|B Chain B, Crystal structure of The Extracellular Domain of Murine Carbonic Anhydrase Xiv
 gi|47168792|pdb|1RJ6|A Chain A, Crystal structure of The Extracellular Domain of Murine Carbonic Anhydrase Xiv In Complex With Acetazolamide
 gi|47168793|pdb|1RJ6|B Chain B, Crystal structure of The Extracellular Domain of Murine Carbonic Anhydrase Xiv In Complex With Acetazolamide
 Length = 261

Score = 438 bits (1127), Expect = e-122
 Identities = 216/261 (82%), Positives = 236/261 (90%)

Query: 18 GGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTEPL 77
 GG HWTYEGPHGQDHP SYPECG +AQSPI+IQTDSV FDPDLPA+QPHGYDQ GTEPL
 Sbjct: 1 GGHHWTYEGPHGQDHWPTSYPECGGDAQSPINIQTDSVIFDPDLPVQPHGYDQLGTEPL 60

Query: 78 DLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGSEHQINSEATFAELHIV 137
 DLHNNGHTVQLSLP TL+LGGLPRKY AAQLHLHWGQ+GS GSEH INSEAT AELH+V
 Sbjct: 61 DLHNNGHTVQLSLPPTLHLGGLPRKYTAAQLHLHWGQRGSLEGSEHHINSEATAAELHV 120

Query: 138 HYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFN 197
 HYDS SY SLSEAA++PQGLAVLGILIEVGET+N AY+HILS LHE+R+KDQKTSVPPF+
 Sbjct: 121 HYDSQSYSSLSEAAQKPQGLAVLGILIEVGETENPAYDHILSR LHEIRYKDQKTSVPPFS 180

Query: 198 LRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSK 257
 +REL P+QL Q+FRYNGSLTTPPCYQSVLWTVF RR+QISM QLEKLQ TL STEE+PS+
 Sbjct: 181 VRELFPQLEQFFRYNGSLTTPPCYQSVLWTVFNRAQISMGGLEKLQETLSSTEEDPSE 240

Query: 258 LLVQNYRALQPLNQRMFASF 278
 LVQNYR QPLNQR +FASF
 Sbjct: 241 PLVQNYRVPQPLNQRRTIFASF 261

Sequences producing significant alignments:			Score (bits)	E Value	
gi 37182499 gb AY358689.1	Homo sapiens clone DNA62812 CA14...	3366	0.0	LU	
gi 6912283 ref NM_012113.1	Homo sapiens carbonic anhydrase...	3350	0.0	LUG	
gi 6009639 dbj AB025904.1	Homo sapiens mRNA for carbonic a...	3350	0.0	LUG	
gi 22760421 dbj AK074765.1	Homo sapiens cDNA FLJ90284 fis,...	3313	0.0	LU	
gi 21706778 gb BC034412.1	Homo sapiens carbonic anhydrase ...	3299	0.0	LUG	
gi 19309420 emb AL138795.21	Human DNA sequence from clone ...	948	0.0		
gi 28422259 gb BC046995.1	Mus musculus carbonic anhydrase ...	805	0.0	LU	
gi 6753263 ref NM_011797.1	Mus musculus carbonic anhydrase...	805	0.0	LUG	
gi 5030907 dbj AB005450.1	Mus musculus mRNA for CA XIV, co...	805	0.0	LUG	
gi 15384634 emb AL451074.13	Human DNA sequence from clone ...	650	0.0	L	
gi 12848980 dbj AK012316.1	Mus musculus 11 days embryo who...	454	e-124	LUG	
gi 34858062 ref XM_342297.1	Rattus norvegicus similar to C...	373	e-100	LU	
gi 15082388 gb BC012108.1	Homo sapiens cDNA clone MGC:2010...	287	4e-74	LUG	
gi 26801277 gb AC092855.39	Mus musculus chromosome 3 clone...	184	4e-43		
gi 26084135 dbj AK034693.1	Mus musculus 12 days embryo emb...	167	1e-37	U	
gi 12844826 dbj AK009805.1	Mus musculus adult male tongue ...	86	3e-13	LUG	
gi 33569140 emb AL845336.9	Mouse DNA sequence from clone R...	74	1e-09		
gi 23334838 gb AC123032.5	Mus musculus BAC clone RP24-480K...	72	4e-09		
gi 46518694 gb AC125192.3	Mus musculus BAC clone RP23-266B...	72	4e-09		
gi 38323102 emb AL954710.27	Mouse DNA sequence from clone ...	70	2e-08		
gi 21955088 gb AC122003.2	Mus musculus BAC clone RP24-336G...	68	7e-08		
gi 3252819 gb AC004382.1	HUAC004382 Homo sapiens Chromosome...	68	7e-08	LUG	
gi 45476650 gb AC122746.7	Mus musculus chromosome 17, clon...	68	7e-08		
gi 4508108 gb AC005101.2	Homo sapiens BAC clone CTA-352J5 ...	68	7e-08	L	
gi 50355915 gb AC124516.4	Mus musculus chromosome 12 clone...	66	3e-07		
gi 50199072 gb AC110559.11	Mus musculus chromosome 7, clon...	66	3e-07		
gi 25046688 gb AC112147.5	Mus musculus BAC clone RP23-175E...	66	3e-07		
gi 37620322 gb AC111047.9	Mus musculus chromosome 3, clone...	66	3e-07		
gi 33590044 gb AC118614.12	Mus musculus chromosome 18, clo...	66	3e-07		
gi 29501916 gb AC099600.5	Mus musculus chromosome 15, clon...	66	3e-07		
gi 33342291 gb AC126722.7	Rattus norvegicus 4 BAC CH230-5L...	66	3e-07		
gi 42475822 emb AL928891.20	Mouse DNA sequence from clone ...	66	3e-07		
gi 47131369 gb AC147160.2	Mus musculus BAC clone RP24-336A...	66	3e-07		
gi 47679190 gb AC109294.8	Mus musculus chromosome 1, clone...	66	3e-07		
gi 15778814 gb AC084382.1	Mus musculus clone RP23-5K17, co...	66	3e-07		
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gi 2687350 gb AF036762.1	MMFGLI2 Mus musculus fibrinogen-l...	66	3e-07		
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gi 22552815 emb AL671984.12	Mouse DNA sequence from clone ...	66	3e-07		
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gi 34495107 gb AC122185.4	Mus musculus BAC clone RP23-18J1...	64	1e-06		
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gi 29135572 gb AC124040.3	Oryctolagus cuniculus clone LB1-...	64	1e-06		
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Strand = Plus / Plus

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Identities = 1698/1701 (99%)
Strand = Plus / Plus

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 Length = 1757

Score = 3350 bits (1690), Expect = 0.0

Identities = 1698/1701 (99%)

Strand = Plus / Plus

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Sbjct: 940 cgctacaatggctcgctcacaactcccccttgctaccagagtgtgctctggacagttttt 999

Query: 961 tatagaaggtcccagatttcaatggaacagctggaaaagcttcaggggacattgttctcc 1020
Sbjct: 1000 tatagaaggtcccagatttcaatggaacagctggaaaagcttcaggggacattgttctcc 1059

Query: 1021 acagaagaggagccctctaagcttctggtacagaactaccgagcccttcagcctctcaat 1080
Sbjct: 1060 acagaagaggagccctctaagcttctggtacagaactaccgagcccttcagcctctcaat 1119

Query: 1081 cagcgcatggtctttgcttctttcatccaagcaggatcctcgataccacaggtgaaatg 1140
Sbjct: 1120 cagcgcatggtctttgcttctttcatccaagcaggatcctcgataccacaggtgaaatg 1179

Query: 1141 ctgagtctaggtgtaggaatcttggttggtgtctctgccttctcctggctgtttatttc 1200
Sbjct: 1180 ctgagtctaggtgtaggaatcttggttggtgtctctgccttctcctggctgtttatttc 1239

Query: 1201 attgctagaaagattcgaagaagaggctggaaaaccgaaagagtgtggtcttcacctca 1260
Sbjct: 1240 attgctagaaagattcgaagaagaggctggaaaaccgaaagagtgtggtcttcacctca 1299

Query: 1261 gcacaagccacgactgaggcataaattccttctcagataccatggatgtggatgacttcc 1320
Sbjct: 1300 gcacaagccacgactgaggcataaattccttctcagataccatggatgtggatgacttcc 1359

Query: 1321 cttcatgcctatcaggaagcctctaaaatggggtgtaggatctggccagaaacactgtag 1380
Sbjct: 1360 cttcatgcctatcaggaagcctctaaaatggggtgtaggatctggccagaaacactgtag 1419

Query: 1381 gagtagtaagcagatgtcctccttccctggacatctcttagagaggaatggaccaggc 1440
Sbjct: 1420 gagtagtaagcagatgtcctccttccctggacatctcttagagaggaatggaccaggc 1479


Query: 1441 tgtcattccaggaagaactgcagagccttcagcctctccaaacatgtaggaggaaatgag 1500
Sbjct: 1480 tgtcattccaggaagaactgcagagccttcagcctctccaaacatgtaggaggaaatgag 1539

Query: 1501 gaaatcgctgtgttggttaatgcagagancaaactctgtttagttgcaggggaagtgtggg 1560
Sbjct: 1540 gaaatcgctgtgttggttaatgcagagaacaaactctgtttagttgcaggggaagtgtggg 1599

Query: 1561 atataccccaagtcctctacccccctcacttttatggccctttccctagatatatactgcgg 1620
Sbjct: 1600 atataccccaagtcctctacccccctcacttttatggccctttccctagatatatactgcgg 1659

Query: 1621 gatctctccttaggataaagagttgctgttggaagttgtatatattttgatcaatatatttg 1680
Sbjct: 1660 gatctctccttaggataaagagttgctgttggaagttgtatatattttgatcaatatatttg 1719

Query: 1681 gaaattaaagtttctgacttt 1701
Sbjct: 1720 gaaattaaagtttctgacttt 1740
```

>gi|22760421|dbj|AK074765.1|  Homo sapiens cDNA FLJ90284 fis, clone NT2RP1000613, weakly si
CARBONIC ANHYDRASE VI (EC 4.2.1.1)
Length = 1771

Score = 3313 bits (1671), Expect = 0.0
Identities = 1682/1686 (99%)
Strand = Plus / Plus

```
Query: 1   gagactgcagagggagataaaagagagagggcaaagaggcagcaagagatttgtcctgggg 60
Sbjct: 86   gagactgcagagggagataaaagagagagggcaaagaggcagcaagagatttgtcctgggg 145

Query: 61   atccagaaacccatgataccctactgaacaccgaatcccctggaagcccacagagacaga 120
Sbjct: 146  atccagaaacccatgataccctactgaacaccgaatcccctggaagcccacagagacaga 205

Query: 121   gacagcaagagaagcagagataaatacactcacgccaggagctcgctcgctctctctctc 180
Sbjct: 206   gacagcaagagaagcagagataaatacactcacgccaggagctcgctcgctctctctctc 265

Query: 181   tctctctcactcctccctccctctctctctgctgtcctagtcctctagtcctcaaattc 240
Sbjct: 266   tctctctcactcctccctccctctctctctgctgtcctagtcctctagtcctcaaattc 325

Query: 241   ccagtcccctgcaccccttcctgggacactatgttgttctccgccctcctgctggagggtg 300
Sbjct: 326   ccagtcccctgcaccccttcctgggacactatgttgttctccgccctcctgctggagggtg 385

Query: 301   atttggatcctggctgcagatgggggtcaacactggacgtatgagggccacatggtcag 360
Sbjct: 386   atttggatcctggctgcagatgggggtcaacactggacgtatgagggccacatggtcag 445

Query: 361   gaccattggccagcctcttaccctgagtgtggaacaatgccagtcgcccacatcgatatt 420
Sbjct: 446   gaccattggccagcctcttaccctgagtgtggaacaatgccagtcgcccacatcgatatt 505

Query: 421   cagacagacagtgtgacatttgaccctgatttgctgctctgcagccccacggatatgac 480
Sbjct: 506   cagacagacagtgtgacatttgaccctgatttgctgctctgcagccccacggatatgac 565

Query: 481   cagcctggcaccgagcctttggacctgcacaacaatggccacacagtgaactctctctg 540
Sbjct: 566   cagcctggcaccgagcctttggacctgcacaacaatggccacacagtgaactctctctg 625

Query: 541   ccctctaccctgtatctgggtggacttccccgaaaatatgtagctgccagctccacctg 600
Sbjct: 626   ccctctaccctgtatctgggtggacttccccgaaaatatgtagctgccagctccacctg 685

Query: 601   cactgggggtcagaaaggatccccaggggggtcagaacaccagatcaacagtgaagccaca 660
Sbjct: 686   cactgggggtcagaaaggatccccaggtgggtcagaacaccagatcaacagtgaagccaca 745

Query: 661   ttgacagagctccacattgtacattatgactctgattcctatgacagcttgagtgaggct 720
Sbjct: 746   ttgacagagctccacattgtacattatgactctgattcctatgacagcttgagtgaggct 805
```

Query: 721 gctgagaggcctcagggcctggctgtcctgggcatcctaattgaggtgggtgagactaag 780

Sbjct: 806 gctgagaggcctcagggcctggctgtcctgggcatcctaattgaggtgggtgagactaag 865

Query: 781 aatatagcttatgaacacattctgagtcacttgcatgaagtcaggcataaagatcagaag 840

Sbjct: 866 aatatagcttatgaacacattctgagtcacttgcatgaagtcaggcataaagatcagaag 925

Query: 841 acctcagtgccctcccttcaacctaagagagctgctccccaacagctggggcagttacttc 900

Sbjct: 926 acctcagtgccctcccttcaacctaagagagctgctccccaacagctggggcagttacttc 985

Query: 901 cgctacaatggctcgctcacaactcccccttgctaccagagtgtgctctggacagttttt 960

Sbjct: 986 cgctacaatggctcgctcacaactcccccttgctaccagagtgtgctctggacagttttt 1045

Query: 961 tatagaaggctccagatttcaatggaacagctggaaaagcttcaggggacattgttctcc 1020

Sbjct: 1046 tatagaaggctccagatttcaatggaacagctggaaaagcttcaggggacattgttctcc 1105

Query: 1021 acagaagaggagccctctaagcttctggtacagaactaccgagcccttcagcctctcaat 1080

Sbjct: 1106 acagaagaggagccctctaagcttctggtacagaactaccgagcccttcagcctctcaat 1165

Query: 1081 cagcgcatggcttttgcttctttcatccaagcaggatcctcgtataccacaggtgaaatg 1140

Sbjct: 1166 cagcgcatggcttttgcttctttcatccaagcaggatcctcgtataccacaggtgaaatg 1225

Query: 1141 ctgagtctaggtgtaggaatcttggttggtgtctctgccttctcctggctgtttatttc 1200

Sbjct: 1226 ctgagtctaggtgtaggaatcttggttggtgtctctgccttctcctggctgtttatttc 1285

Query: 1201 attgctagaaagattcggaagaagaggctggaaaaccgaaagagtgtggtcttcacctca 1260

Sbjct: 1286 attgctagaaagattcggaagaagaggctggaaaaccgaaagagtgtggtcttcacctca 1345

Query: 1261 gcacaagccacgactgaggcataaattccttctcagataccatggatgtggatgacttcc 1320

Sbjct: 1346 gcacaagccacgactgaggcataaattccttctcagataccatggatgtggatgacttcc 1405

Query: 1321 cttcatgcctatcaggaagcctctaaaatggggtgtaggatctggccagaaacactgtag 1380

Sbjct: 1406 cttcatgcctatcaggaagcctctaaaatggggtgtaggatctggccagaaacactgtag 1465

Query: 1381 gagtagtaagcagatgtcctccttccccctggacatctcttagagaggaatggaccaggc 1440

Sbjct: 1466 gagtagtaagcagatgtcctccttccccctggacatctcttagagaggaatggaccaggc 1525

Query: 1441 tgtcattccaggaagaactgcagagccttcagcctctccaaacatgtaggaggaaatgag 1500

Sbjct: 1526 tgtcattccaggaagaactgcagagccttcagcctctccaaacatgtaggaggaaatgag 1585

Query: 1501 gaaatcgctgtgttggttaatgcagagancaaactctgtttagttgcaggggaagtttggg 1560

Sbjct: 1586 gaaatcgctgtgttggttaatgcagagaacaaactctgtttagttgcaggggaagtttggg 1645

Query: 1561 atatacccccagtcctctacccccctcacttttatggccctttccctagatatactgcgg 1620

Sbjct: 1646 atatacccccagtcctctacccccctcacttttatggccctttccctagatataactgcgg 1705

Query: 1621 gatctctccttaggataaaagagttgctgttgaagttgtatattttgatcaatatatttg 1680

Sbjct: 1706 gatctctccttaggataaaagagttgctgttgaagttgtatattttgatcaatatatttg 1765

Query: 1681 gaaatt 1686

Sbjct: 1766 gaaatt 1771

>gi|21706778|gb|BC034412.1| **LOC** Homo sapiens carbonic anhydrase XIV, mRNA (cDNA clone MGC:34
IMAGE:5175251), complete cds
Length = 1767

Score = 3299 bits (1664), Expect = 0.0

Identities = 1669/1671 (99%)

Strand = Plus / Plus

Query: 31 caaagaggcagcaagagatttgcctggggatccagaaacccatgataccctactgaaca 90

Sbjct: 1 caaagaggcagcaagagatttgcctggggatccagaaacccatgataccctactgaaca 60

Query: 91 ccgaatcccctggaagcccacagagacagagacagcaagagaagcagagataaatacact 150

Sbjct: 61 ccgaatcccctggaagcccacagagacagagacagcaagagaagcagagataaatacact 120

Query: 151 cacgccaggagctcgctcgctctctctctctctctcactcctccctcctctctctct 210

Sbjct: 121 cacgccaggagctcgctcgctctctctctctctctcactcctccctcctctctctct 180

Query: 211 gcctgtccttagtcctctagtcctcaaattcccagtcctcctgcaccccttcctgggacact 270

Sbjct: 181 gcctgtccttagtcctctagtcctcaaattcccagtcctcctgcaccccttcctgggacact 240

Query: 271 atgttggttctccgccctcctgctggaggtgatttggatcctggctgcagatgggggtcaa 330

Sbjct: 241 atgttggttctccgccctcctgctggaggtgatttggatcctggctgcagatgggggtcaa 300

Query: 331 cactggacgtatgagggcccacatggtcaggaccattggccagcctcttaccctgagtgt 390

Sbjct: 301 cactggacgtatgagggcccacatggtcaggaccattggccagcctcttaccctgagtgt 360

Query: 391 ggaaacaatgccagtcgcccacatcgatattcagacagacagtgtagacatttgaccctgat 450

Sbjct: 361 ggaaacaatgccagtcgcccacatcgatattcagacagacagtgtagacatttgaccctgat 420

Query: 451 ttgcctgctctgcagccccacggatatgaccagcctggcaccgagcctttggacctgcac 510

Sbjct: 421 ttgcctgctctgcagccccacggatatgaccagcctggcaccgagcctttggacctgcac 480

Query: 511 aacaatggccacacagtgcaactctctctgccctctaccctgtatctgggtggacttccc 570

Sbjct: 481 aacaatggccacacagtgcaactctctctgccctctaccctgtatctgggtggacttccc 540

Query: 571 cgaaaaatatgtagctgccagctccacctgcactgggggtcagaaaggatccccagggggg 630

Sbjct: 541 cgaaaaatatgtagctgccagctccacctgcactgggggtcagaaaggatccccagggggg 600

Query: 631 tcagaacaccagatcaacagtgaagccacatttgcagagctccacattgtacattatgac 690
Sbjct: 601 tcagaacaccagatcaacagtgaagccacatttgcagagctccacattgtacattatgac 660

Query: 691 tctgattcctatgacagcttgagtgaaggctgctgagaggcctcagggcctggctgtcctg 750
Sbjct: 661 tctgattcctatgacagcttgagtgaaggctgctgagaggcctcagggcctggctgtcctg 720

Query: 751 ggcatcctaattgaggtgggtgagactaagaatatagcttatgaacacattctgagtcac 810
Sbjct: 721 ggcatcctaattgaggtgggtgagactaagaatatagcttatgaacacattctgagtcac 780

Query: 811 ttgcatgaagtcaggcataaagatcagaagacctcagtgccctccctcaacctaagagag 870
Sbjct: 781 ttgcatgaagtcaggcataaagatcagaagacctcagtgccctccctcaacctaagagag 840

Query: 871 ctgctccccaacagctggggcagctacttccgctacaatggctcgctcacaactccccct 930
Sbjct: 841 ctgctccccaacagctggggcagctacttccgctacaatggctcgctcacaactccccct 900

Query: 931 tgctaccagagtgctgctctggacagttttttatagaaggctccagatttcaatggaacag 990
Sbjct: 901 tgctaccagagtgctgctctggacagttttttatagaaggctccagatttcaatggaacag 960

Query: 991 ctggaaaagcttcaggggacattgttctccacagaagaggagccctctaagcttctggta 1050
Sbjct: 961 ctggaaaagcttcaggggacattgttctccacagaagaggagccctctaagcttctggta 1020

Query: 1051 cagaactaccgagcccttcagcctctcaatcagcgcatggctcttgcttcttcatccaa 1110
Sbjct: 1021 cagaactaccgagcccttcagcctctcaatcagcgcatggctcttgcttcttcatccaa 1080

Query: 1111 gcaggatcctcgatataccacaggtgaaatgctgagcttaggtgtaggaatcttggttggc 1170
Sbjct: 1081 gcaggatcctcgatataccacaggtgaaatgctgagcttaggtgtaggaatcttggttggc 1140

Query: 1171 tgtctctgccttctcctggctgtttatttcattgctagaaagattcggaagaagaggctg 1230
Sbjct: 1141 tgtctctgccttctcctggctgtttatttcattgctagaaagattcggaagaagaggctg 1200

Query: 1231 gaaaaccgaaagagtgtggtcttcacctcagcacaagccacgactgaggcataaattcct 1290
Sbjct: 1201 gaaaaccgaaagagtgtggtcttcacctcagcacaagccacgactgaggcataaattcct 1260

Query: 1291 tctcagataccatggatgtggatgacttcccttcatgcctatcaggaagcctctaaaatg 1350
Sbjct: 1261 tctcagataccatggatgtggatgacttcccttcatgcctatcaggaagcctctaaaatg 1320

Query: 1351 ggggtgtaggatctggccagaaacactgtaggagtagtaagcagatgtcctccttcccctg 1410
Sbjct: 1321 ggggtgtaggatctggccagaaacactgtaggagtagtaagcagatgtcctccttcccctg 1380

Query: 1411 gacatctcttagagaggaatggaccaggctgtcattccaggaagaactgcagagccttc 1470
Sbjct: 1381 gacatctccttagagaggaatggaccaggctgtcattccaggaagaactgcagagccttc 1440

Query: 1471 agcctctccaaacatgtaggaggaaatgaggaaatcgctgtgttgttaatgcagaganca 1530

|||||
Sbjct: 1441 agcctctccaaacatgtaggaggaaatgaggaaatcgctgtgttattaatgcagagaaca 1500

Query: 1531 aactctgtttagttgcaggggaagtttgggatataaccccaaagtcctctacccccctcact 1590


|||||
Sbjct: 1501 aactctgtttagttgcaggggaagtttgggatataaccccaaagtcctctacccccctcact 1560

Query: 1591 tttatggccctttccctagatataactgcgggatctctccttaggataaagagttgctgtt 1650

|||||
Sbjct: 1561 tttatggccctttccctagatataactgcgggatctctccttaggataaagagttgctgtt 1620

Query: 1651 gaagttgtatatattttgatcaatatatttggaaattaaagtttctgacttt 1701

|||||
Sbjct: 1621 gaagttgtatatattttgatcaatatatttggaaattaaagtttctgacttt 1671

>gi|19309420|emb|AL138795.21|  Human DNA sequence from clone RP4-790G17 on chromosome 1q21.1-
complete sequence
Length = 132823

Score = 948 bits (478), Expect = 0.0

Identities = 483/485 (99%)

Strand = Plus / Plus

Query: 1217 ggaagaagaggctggaaaaccgaaagagtgtggtcttcacctcagcacaagccacgactg 1276

|||||
Sbjct: 78784 ggaagaagaggctggaaaaccgaaagagtgtggtcttcacctcagcacaagccacgactg 78843

Query: 1277 aggcataaattccttctcagataccatggatgtggatgacttccttcatgcctatcagg 1336

|||||
Sbjct: 78844 aggcataaattccttctcagataccatggatgtggatgacttccttcatgcctatcagg 78903

Query: 1337 aagcctctaaaatgggggtgtaggatctggccagaaacactgtaggagtagtaagcagatg 1396

|||||
Sbjct: 78904 aagcctctaaaatgggggtgtaggatctggccagaaacactgtaggagtagtaagcagatg 78963

Query: 1397 tcctccttcccctggacatctccttagagaggaatggaccaggctgtcattccaggaaga 1456

|||||
Sbjct: 78964 tcctccttcccctggacatctccttagagaggaatggaccaggctgtcattccaggaaga 79023

Query: 1457 actgcagagccttcagcctctccaaacatgtaggaggaaatgaggaaatcgctgtgttgt 1516

|||||
Sbjct: 79024 actgcagagccttcagcctctccaaacatgtaggaggaaatgaggaaatcgctgtgttgt 79083

Query: 1517 taatgcagagancaaactctgttttagttgcaggggaagtttgggatataaccccaaagtcc 1576

|||||
Sbjct: 79084 taatgcagagaacaaactctgttttagttgcaggggaagtttgggatataaccccaaagtcc 79143

Query: 1577 tctacccccctcacttttatggccctttccctagatataactgcgggatctctccttaggat 1636

|||||
Sbjct: 79144 tctacccccctcacttttatggccctttccctagatataactgcgggatctctccttaggat 79203

Query: 1637 aaagagttgctgttgaagttgtatatattttgatcaatatatttggaaattaaagtttctg 1696

|||||
Sbjct: 79204 aaagagttgctgttgaagttgtatatattttgatcaatatatttggaaattaaagtttctg 79263

Query: 1697 acttt 1701

|||||
Sbjct: 79264 acttt 79268

7/26/04

Sbjct: 77231 agatcagaagacctcagtcgctcccttcaacctaagagagctgctccccaacagctggg 77290

Query: 891 gcagtacttccgctacaatggctcgctcacaactcccccttgctaccagagtgtgctctg 950
|||||
Sbjct: 77291 gcagtacttccgctacaatggctcgctcacaactcccccttgctaccagagtgtgctctg 77350

Query: 951 gacagttttttatagaagggtcccagatttcaatggaacag 990
|||||
Sbjct: 77351 gacagttttttatagaagggtcccagatttcaatggaacag 77390

Score = 293 bits (148), Expect = 6e-76
Identities = 148/148 (100%)
Strand = Plus / Plus

Query: 522 cacagtgcgaactctctctgccctctaccctgtatctgggtggacttccccgaaaatatgt 581
|||||
Sbjct: 76344 cacagtgcgaactctctctgccctctaccctgtatctgggtggacttccccgaaaatatgt 76403

Query: 582 agctgccagctccacctgcactgggggtcagaaaggatccccaggggggtcagaacacca 641
|||||
Sbjct: 76404 agctgccagctccacctgcactgggggtcagaaaggatccccaggggggtcagaacacca 76463

Query: 642 gatcaacagtgaagccacatttgcagag 669
|||||
Sbjct: 76464 gatcaacagtgaagccacatttgcagag 76491

Score = 246 bits (124), Expect = 1e-61
Identities = 124/124 (100%)
Strand = Plus / Plus

Query: 988 cagctggaaaagcttcaggggacattgttctccacagaagaggagccctctaagcttctg 1047
|||||
Sbjct: 77487 cagctggaaaagcttcaggggacattgttctccacagaagaggagccctctaagcttctg 77546

Query: 1048 gtacagaactaccgagcccttcagcctctcaatcagcgcattggtctttgcttctttcatc 1107
|||||
Sbjct: 77547 gtacagaactaccgagcccttcagcctctcaatcagcgcattggtctttgcttctttcatc 77606

Query: 1108 caag 1111
|||||
Sbjct: 77607 caag 77610

Score = 198 bits (100), Expect = 3e-47
Identities = 100/100 (100%)
Strand = Plus / Plus

Query: 668 agctccacattgtacattatgactctgattcctatgacagcttgagtgaggctgctgaga 727
|||||
Sbjct: 76714 agctccacattgtacattatgactctgattcctatgacagcttgagtgaggctgctgaga 76773

Query: 728 ggcctcagggcctggctgtcctgggcatcctaattgaggt 767
|||||
Sbjct: 76774 ggcctcagggcctggctgtcctgggcatcctaattgaggt 76813

Score = 176 bits (89), Expect = 1e-40

Identities = 89/89 (100%)

Strand = Plus / Plus

Query: 1130 cagggtgaaatgctgagcttaggtgtaggaatcttggttggtgctgtctctgccttctcctgg 1189
|||||
Sbjct: 77982 cagggtgaaatgctgagcttaggtgtaggaatcttggttggtgctgtctctgccttctcctgg 78041

Query: 1190 ctgtttatttcattgctagaaagattcgg 1218
|||||
Sbjct: 78042 ctgtttatttcattgctagaaagattcgg 78070

Score = 137 bits (69), Expect = 9e-29

Identities = 69/69 (100%)

Strand = Plus / Plus

Query: 764 aggtgggtgagactaagaatatagcttatgaacacattctgagtcacttgcatagaagtca 823
|||||
Sbjct: 76993 aggtgggtgagactaagaatatagcttatgaacacattctgagtcacttgcatagaagtca 77052

Query: 824 ggcataaag 832
|||||
Sbjct: 77053 ggcataaag 77061

Score = 50.1 bits (25), Expect = 0.016

Identities = 25/25 (100%)

Strand = Plus / Plus


Query: 1110 agcaggatcctcgtataccacaggt 1134
|||||
Sbjct: 77848 agcaggatcctcgtataccacaggt 77872

Score = 46.1 bits (23), Expect = 0.25

Identities = 23/23 (100%)

Strand = Plus / Plus

Query: 325 ggtcaacactggacgtatgaggg 347
|||||
Sbjct: 74337 ggtcaacactggacgtatgaggg 74359

>[gi|28422259|gb|BC046995.1](#)  Mus musculus carbonic anhydrase 14, mRNA (cDNA clone MGC:54680 IMAGE:6491779), complete cds
Length = 1654

Score = 805 bits (406), Expect = 0.0

Identities = 844/990 (85%)

Strand = Plus / Plus

Query: 270 tatgttggttctccgccctcctgctggaggtgatttggatcctggctgcagatgggggtca 329
|||||
Sbjct: 247 tatgttggttctcgtctcctgttaaagggtgacttggatcctggctgcagatgggggtca 306

Query: 330 aactggacgtatgagggccacatgggtcaggaccattggccagcctcttaccctgagtg 389
|||||
Sbjct: 307 ccactggacatatgaaggccacacgggtcaggaccattggccaacctcttatcctgagtg 366

7/26/04

sbjct: 985 gttagagaagctccaggagacattgtcctctacagaagaggacccctctgagccccttgt 1044

sbjct: 1045 acagaactacagagtccccagcctctcaaccagaggaccatctttgcttctttcatcca 1104

sbjct: 1105 agcaggaccactgtataccacaggagagatgctgggtctaggtgtgggaatcttggctgg 1164

sbjct: 1165 atgtccttgcccttctgctggctgtttatttcacgctcaaaaaattaggaagaagcggct 1224

sbjct: 1225 gggaaacaggaaaagtgtggttttcacctc 1254

LEO

Score = 805 bits (406), Expect = 0.0
Identities = 844/990 (85%)
Strand = Plus / Plus

sbjct: 265 tatgttggttcttcgctctcctgttaaagggtgacttggatcctggctgcagatgggggtca 324

sbjct: 325 ccactggacatatgaaggccacacggtcaggaccattggccaacctcttattcctgagtg 384

sbjct: 385 tggaggcgatgccagtcctccatcaatatccagacagacagtgtgatatttgaccccgga 444

sbjct: 445 tctgcctgctgtacagcccatggatatgaccagcttgggactgagcctttggatctaca 504

sbjct: 505 caataatggccatacagtgacagctttccctgcccccaaccctgcacctgggtggactgcc 564

sbjct: 565 ccgaaaatacacagcagcccagctccacctgcactgggggtcagagaggatccctcgaggg 624

sbjct: 625 atcagagcaccagatcaacagtgaagccacggctgcggagctccacgtggttcactatga 684

[illegible]

Sbjct: 685 ctcccagtcctacagcagcttgagtgaggcagctcagaagccacagggcctggctgtcct 744

Query: 750 gggcatcctaattgaggtgggtgagactaagaatatagcttatgaacacattctgagtca 809

Sbjct: 745 aggcattcctcattgaggtgggcgagactgagaatccagcttatgatcacattctgagtcg 804

Query: 810 cttgcatgaagtcaggcataaagatcagaagacctcagtcctcccttcaacctaagaga 869

Sbjct: 805 tctacatgaaataagatacaaagatcagaagacctctgtgcctcccttcagcgtgagaga 864

Query: 870 gctgctccccaacagctggggcagtacttccgctacaatggctcgctcacaactcccc 929

Sbjct: 865 gctgttccccaacagctggagcaattcttccgctacaacggctcactcacaactcccc 924

Query: 930 ttgctaccagagtgtgctctggacagtttttatagaaggtcccagatttcaatggaaca 989

Sbjct: 925 ctgctaccagagtgtgctctggacagtcttcaacagaagggccagatttcaatgggaca 984

Query: 990 gctggaaaagcttcaggggacattgttctccacagaagaggagccctctaagcttctggt 1049

Sbjct: 985 gttagagaagctccaggagacattgtcctctacagaagaggacccctctgagcccttgt 1044

Query: 1050 acagaactaccgagcccttcagcctctcaatcagcgcatggtctttgcttctttcatcca 1109

Sbjct: 1045 acagaactacagagtccccagcctctcaaccagaggaccatctttgcttctttcatcca 1104

Query: 1110 agcaggatcctcgtataccacaggtgaaatgctgagtcctaggtgtaggaatcttggttg 1169

Sbjct: 1105 agcaggaccactgtataccacaggagagatgctgggtctaggtgtgggaatcttggttg 1164

Query: 1170 ctgtctctgccttctcctggctgtttatttcattgctagaaagattcggaagaaggct 1229

Sbjct: 1165 atgtctttgccttctgctggctgtttatttcattgctcaaaaaattaggaagaagcggct 1224

Query: 1230 ggaaaaccgaaagagtgtggtcttcacctc 1259

Sbjct: 1225 gggaaacaggaaaagtgtggttttcacctc 1254

>gi|6912284|ref|NP_036245.1| carbonic anhydrase XIV precursor; carbonic dehydratase [Homo sapiens]

gi|8928036|sp|Q9ULX7|CAHE_HUMAN Carbonic anhydrase XIV precursor (Carbonate dehydratase XIV (CA-XIV) (UNQ690/PRO1335)

gi|6009640|dbj|BAA85002.1| carbonic anhydrase 14 [Homo sapiens]

gi|21706779|gb|AAH34412.1| Carbonic anhydrase XIV, precursor [Homo sapiens]

gi|37182500|gb|AAQ89052.1| CA14 [Homo sapiens]

Length = 337

Score = 682 bits (1760), Expect = 0.0

Identities = 337/337 (100%), Positives = 337/337 (100%)

```

Query: 1  MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60
          MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD
Sbjct: 1  MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60

Query: 61  LPALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120
          LPALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG
Sbjct: 61  LPALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120

Query: 121 SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180
          SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH
Sbjct: 121 SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180

Query: 181 LHEVRHKDQKTSVPPFNRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240
          LHEVRHKDQKTSVPPFNRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ
Sbjct: 181 LHEVRHKDQKTSVPPFNRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240

Query: 241 LEKLQGTFLSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVG 300
          LEKLQGTFLSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVG
Sbjct: 241 LEKLQGTFLSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVG 300

Query: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337
          CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA
Sbjct: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337

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>gi|22760422|dbj|BAC11191.1| unnamed protein product [Homo sapiens]

Length = 337

Score = 681 bits (1756), Expect = 0.0

Identities = 336/337 (99%), Positives = 336/337 (99%)

```

Query: 1  MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60
          MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD
Sbjct: 1  MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPD 60

Query: 61  LPALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120
          LPALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG
Sbjct: 61  LPALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPG 120

Query: 121 SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180
          SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH
Sbjct: 121 SEHQINSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSH 180

Query: 181 LHEVRHKDQKTSVPPFNRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240
          LHEVRHKDQKTSVPPFNRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ
Sbjct: 181 LHEVRHKDQKTSVPPFNRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQ 240

Query: 241 LEKLQGTFLSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVG 300
          LEKLQGTFLSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVG
Sbjct: 241 LEKLQGTFLSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVG 300

Query: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337
          CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA
Sbjct: 301 CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA 337

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7/26/04

7/26/04

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|||||
Sbjct: 880 acctcagtgctcccttcaacctaagagagctgctccccaacagctggggcagtacttc 939

Query: 901 cgctacaatggctcgctcacaactcccccttgctaccagagtgtgctctggacagttttt 960
Sbjct: 940 cgctacaatggctcgctcacaactcccccttgctaccagagtgtgctctggacagttttt 999

Query: 961 tatagaaggtcccagatttcaatggaacagctggaaaagcttcaggggacattgttctcc 1020
Sbjct: 1000 tatagaaggtcccagatttcaatggaacagctggaaaagcttcaggggacattgttctcc 1059

Query: 1021 acagaagaggagccctctaagcttctggtacagaactaccgagcccttcagcctctcaat 1080
Sbjct: 1060 acagaagaggagccctctaagcttctggtacagaactaccgagcccttcagcctctcaat 1119

Query: 1081 cagcgcatggtctttgcttctttcatccaagcaggatcctcgataaccacaggtgaaatg 1140
Sbjct: 1120 cagcgcatggtctttgcttctttcatccaagcaggatcctcgataaccacaggtgaaatg 1179

Query: 1141 ctgagtctaggtgtaggaatcttggttggtgtctctgccttctcctggctgtttatttc 1200
Sbjct: 1180 ctgagtctaggtgtaggaatcttggttggtgtctctgccttctcctggctgtttatttc 1239

Query: 1201 attgctagaaagattcggaagaagaggctggaaaaccgaaagagtgtggtcttcacctca 1260
Sbjct: 1240 attgctagaaagattcggaagaagaggctggaaaaccgaaagagtgtggtcttcacctca 1299

Query: 1261 gcacaagccacgactgaggcataaattccttctcagataccatggatgtggatgacttcc 1320
Sbjct: 1300 gcacaagccacgactgaggcataaattccttctcagataccatggatgtggatgacttcc 1359

Query: 1321 cttcatgcctatcaggaagcctctaaaatggggtgtaggatctggccagaaacactgtag 1380
Sbjct: 1360 cttcatgcctatcaggaagcctctaaaatggggtgtaggatctggccagaaacactgtag 1419

Query: 1381 gagtagtaagcagatgtcctccttcccctggacatctcttagagaggaatggaccaggc 1440
Sbjct: 1420 gagtagtaagcagatgtcctccttcccctggacatctcttagagaggaatggaccaggc 1479

Query: 1441 tgtcattccaggaagaactgcagagccttcagcctctccaaacatgtaggaggaaatgag 1500
Sbjct: 1480 tgtcattccaggaagaactgcagagccttcagcctctccaaacatgtaggaggaaatgag 1539

Query: 1501 gaaatcgctgtgttggttaatgcagagancaaactctgtttagttgcaggggaagtttggg 1560
Sbjct: 1540 gaaatcgctgtgttggttaatgcagagaacaaactctgtttagttgcaggggaagtttggg 1599

Query: 1561 atataccccaagtcctctaccccctcacctttatggccctttccctagatatactgcgg 1620
Sbjct: 1600 atataccccaagtcctctaccccctcacctttatggccctttccctagatatactgcgg 1659

Query: 1621 gatctctccttaggataaagagttgctgttggaagttgtatatttttgatcaatatatttg 1680
Sbjct: 1660 gatctctccttaggataaagagttgctgttggaagttgtatatttttgatcaatatatttg 1719

Query: 1681 gaaattaaagtttctgacttt 1701
Sbjct: 1720 gaaattaaagtttctgacttt 1740
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